The genetic structuring of Atlantic salmon (Salmo salar L.) populations in northwest Europe as revealed through nuclear microsatellite and mtDNA PCR-RFLP analysis:

From regional to catchment level analysis and its application in conservation and management of the species.

In the style of the Journal of Fish Biology.

Submitted by Anna Kathryn Finnegan to the University of Exeter as a thesis for the degree of Doctor of Philosophy in Biological Sciences, June 2009.

I certify that all material in this thesis which is not my own work has been identified and that no material has previously been submitted and approved for the award of a degree by this or any other University.

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ABSTRACT

The structuring of Atlantic salmon (Salmo salar L.) into discrete, genetically differentiated populations both within and between river catchments is well documented. The utilisation of this knowledge has proved valuable in a variety of evolutionary, ecological, managerial and conservation contexts. In this thesis, the genetic structuring of Atlantic salmon populations in northwest Europe was assessed in two catchments of very different sizes, using a range of molecular and associated population genetic methods; findings from the catchment level research are set in context by a broader phylogeographic study of post-glacial colonisation of the region.

A regional study into the glacial origins and post-glacial colonisation routes of Atlantic salmon in northwest Europe was explored by analysing a pre-existing microsatellite dataset and supplementing it with haplotype data from mtDNA PCR-RFLP analysis of the same samples (N=702). Evidence from allele permutation tests undertaken on the microsatellite data alongside mtDNA haplotype frequencies suggested that there was a cryptic northern refuge in northwest France, with colonisation of the British Isles and Ireland occurring from this and the long-known Iberian Peninsula refuge.

Catchment level studies were undertaken on the river Dart and river Tweed, involving 1151 fish being genotyped with 14 microsatellite loci with a subset of 211 fish being genotyped by mtDNA PCR-RFLP. In both catchments, populations were found to be weakly differentiated genetically, and were most consistent with the meta-population theory of evolution. Similarly, individual spatial autocorrelation analysis indicated that each major tributary within the catchments could be considered as a distinct management or conservation unit. In the Tweed dataset, however, limitations in the sample coverage across the catchment reduced the robustness of some findings.

Historical stocking of the river Dart with fish from Scotland and Iceland is well-documented. The long-term implications of these activities on contemporary Dart populations were assessed by genotyping 177 fish from the donor populations using scale samples taken in the 1960s and comparing them to contemporary Dart populations by undertaking admixture analysis. Overall, admixture between the

donor and recipient populations was low and appeared to reflect natural underlying levels of genetic relationships. However, increased admixture of donor stocks with one extant Dart population was apparent, indicating some potentially long-term localised success of the stocked fish through hybridisation with the native populations; nevertheless, with the population continuing to decline, this should not be viewed as a successful supplementation programme.

Two tributaries on the river Tweed, the Gala and Leader, were inaccessible to salmon for long periods due to the construction of barriers to migration. On both tributaries, fish passes were installed in the 1940s and re-colonisation of the tributaries was possible. Assignment analysis was undertaken and indicated that, contrary to findings for between catchment studies, salmon straying from the most proximate tributaries (i.e. the Ettrick and Caddon) did not appear to be the principal colonisers of the current Gala and Leader populations. Rather, the highest proportion of Gala samples assigned to the Teviot (42%), with the Leader populations assigning to many tributaries across the catchment (Ettrick 28%; Upper 21%; Teviot 19%). However, given the relatively weak differentiation of the baseline samples and limitations inherent in the dataset, the correct self-assignment of baseline samples was very low (average 26%; range 0-47%), hence interpretation must be undertaken with caution. Nevertheless, the findings suggest that the Gala population may have reached a temporally stable state in the 60 years since it has been accessible to salmon.

Whilst the relatively small scale of these studies is acknowledged, the application of the findings in management and conservation of the species are discussed in a wider context. These studies would support the following recommendations: to include information on the historic (refugial) origin of contemporary populations in regional management strategies; to treat each major tributary as a distinct unit as an appropriate scale for catchment level management; and, with stocking and supplementation programmes appearing to have no significant long-term success, coupled with the relative speed with which extirpated tributaries appear to be naturally re-colonised, the use of stocking and supplementation programmes should be discouraged.

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